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RESULT 2
ID Y021-STNY3 STANDARD: PRT: 277 AA.
AC Q55682;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE PUTATIVE PROTEASE SLR0021 (EC 3.4.-.-).
GN SLR0021.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96127529.
RA KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
RA SUGIURA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome."
RL DNA RES. 2:153-166(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U7.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC -----
CC DR EMBL: D64000; G1001581;
CC PFAM: PF01343; Peptidase U7; 1.
CC KW HYPOTHETICAL PROTEIN; HYDROLASE; PROTEASE.
CC SEQUENCE 277 AA: 30274 MW: E996320D CRC32:

Query Match 15.7%: Score 94; DB 1: Length 277;
Best Local Similarity 39.4%: Pred. No. 3.43e-01;
Matches 13; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Db 120 LLEKGVSEK-VIKSGPKYDILSPRELLPEQ 151
39 LLEKDMAFQELADPGPFGSPFAQELDDQ 71

RESULT 3
ID YBBB-ECOLI STANDARD: PRT: 364 AA.
AC P33667; P77709;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 41.1 KD PROTEIN IN RHD-GCL INTERGENIC REGION.
GN YBBB.
OS ESCHERICHTIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE: 9742661.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLIADO-VIDES J., GLASNER F.D., RODE C.R., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RT SCIENCE 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RC ROBERTS D., ALLEN E., ARAUJO R., APARICIO A., CHUNG E., DAVIS K.,
RA DUNCAN M., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O.,
RA LEW H., LIN D., NAKATH A., OEFNER P., SCHRAMM S., DAVIS R.W.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 268-364 FROM N.A.

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RC STRAIN-K12;
RX MEDLINE: 92115567.
RA SADOSKY A.B., GRAY J.A., HILL C.W.;
RT "The Rhd-E subfamily of Escherichia coli K-12."
RL NUCLEIC ACIDS RES. 19:7177-7183(1991).
CC -----
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CC -----
CC DR EMBL: AE000156; G1786712;
CC DR EMBL: U82664; G1773184;
CC DR EMBL: L19084; G304940;
CC DR ECOGENE: EC11768; YBBB.
CC KW HYPOTHETICAL PROTEIN; ATP-BINDING.
CC NP_BIND 149 156
CC SEQUENCE 364 AA: 41110 MW: DA776C59 CRC32:

Query Match 15.7%: Score 94; DB 1: Length 364;
Best Local Similarity 39.4%: Pred. No. 3.43e-01;
Matches 13; Conservative 10; Mismatches 8; Indels 2; Gaps 2;

Db 298 YNELAARLDAALTLQTGTGTHLAVPLLE 330
11 FGLPDLHAQLR-DLTSSSD-ELSWIETLE 41

RESULT 4
ID SYAC-YEAST STANDARD: PRT: 958 AA.
AC P40825;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ALANYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.7) (ALANINE--TRNA
DE LIGASE) (ALARS).
GN ALA1 OR YOR335C.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RA RIMMASTER T.L., SCHIMMEL P.;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97051586.
RA PARLE-MCDERMOTT A.G., HAND N.J., GOULDING S.G., WOLFE K.H.;
RT "Sequence of 29 kb around the PD10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I."
RL YEAST 12:999-1004(1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-ALANINE + TRNA(ALA) -> AMP +
CC PYROPHOSPHATE + L-ALANYL-TRNA(ALA).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC DR EMBL: U18672; G609338;
CC DR EMBL: Z49821; E218690;
CC DR EMBL: Z75243; E252159;
CC DR SGD: L0002757; ALA1.
CC PROSITE: PS00179; AA-TRNA_LIGASE_II_1; FALSE_NEG.

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Query Match 14.9% Score 89; DB 1; Length 952;
Best Local Similarity 32.7% Pred. No. 1.52e+00;
Matches 16; Conservative 15; Mismatches 15; Indels 3; Gaps 3;

Db 772 MDLTPSEETLESVELLNTWGEOPETDSFTGATLEGSLDLSLF 820

Qy 22 LRDLTSSSDSE-LSWITELLEGKMAFO-EALDPGPF-DGSPFAOELL 67

RESULT 9
ID YGFB_ECOLI STANDARD; PRT: 194 AA.
AC P25533;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOHETICAL 21.5 KD PROTEIN IN PEPP-SSR INTERGENIC REGION (ORF194)
DE (F194).
GN YGFB.
OS ESCHERICHIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-HB101.
RX MEDLINE: 930534351.
RA NAKAHIGASHI K., MIYAMOTO K., NISHIMURA K., INOKUCHI H.;
RT "Isolation and characterization of a light-sensitive mutant of
RT Escherichia coli K-12 with a mutation in a gene that is required for
RT the biosynthesis of ubiquinone."
RL J. BACTERIOL. 174:7352-7359(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE: 97426617.
RA BLATTNER F.R., PLUNKETT J., BLOCH C.A., PERA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RT SCIENCE 277:1453-1474(1997).
CC -1- SIMILARITY: STRONG, TO H.INFLUENZA H10817.

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CC EMBL: D90281; G216626;
DR EMBL: U28377; G882439;
DR EMBL: AE000374; G1789276;
DR PIR: J00842; J00842;
DR PIR: A47020; A47020;
DR ECOGENE: EG11323; YGFB.
KW HYPOHETICAL PROTEIN.
SQ SEQUENCE 194 AA; 21474 MW; 104C05A8 CRC32;

Query Match 14.7% Score 88; DB 1; Length 194;
Best Local Similarity 28.6% Pred. No. 2.04e+00;
Matches 16; Conservative 16; Mismatches 22; Indels 2; Gaps 1;

Db 30 EMHGLTSGMTCGNDSSWPLJLHDLTNEGMAHCHLAOLRMHMSATSDALDDG 85
Qy 17 QLMHQLDLTSSSDSELSWITEL-LEKDMAQOALDPGPFDOGSPFAOELLDDG 70

RESULT 10
ID RPEP_ALCEU STANDARD; PRT: 241 AA.
AC 004539;
DT 01-FEB-1995 (REL. 31, CREATED)

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE RIBULOSE-PHOSPHATE 3-EPIMERASE, PLASMID (EC 5.1.3.1) (PENTOSE-5-
DE PHOSPHATE 3-EPIMERASE) (PPE) (R5P3E).
GN CBEP OR CPEX.

OS ALCALIGENES EUTROPHUS.
OG PLASMID MEGAPLASMID PHG1.
OC BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; BURKHOLDERIA GROUP;
OC RALSTONIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-H16 / ATCC 17699;
RX MEDLINE: 930534349.
RA KUSTAN B., YOO J.-G., BEDNARSKI R., BOWEN B.;

RT "The Calvin cycle enzyme pentose-5-phosphate 3-epimerase is encoded
RT within the cfx operons of the chemolithotroph Alcaligenes eutrophus."
RL J. BACTERIOL. 174:7337-7344(1992).
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 5-PHOSPHATE -> D-XYLULOSE 5-
CC PHOSPHATE.

CC -1- PATHWAY: CALVIN CYCLE.
CC -1- SIMILARITY: BELONGS TO THE RIBULOSE-PHOSPHATE 3-EPIMERASE FAMILY.
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DR EMBL: M64172; G150678;
DR PROSITE: PS01085; RIBUL_P_3-EPIMER_1; 1.
DR PROSITE: PS01086; RIBUL_P_3-EPIMER_2; 1.
DR PFAM: PF00834; Ribul_P_3-epim; 1.
KW ISOMERASE; CARBOHYDRATE METABOLISM; CALVIN CYCLE; PLASMID.
SQ SEQUENCE 241 AA; 25594 MW; 4F4B48CD CRC32;

Query Match 14.7% Score 88; DB 1; Length 241;
Best Local Similarity 30.6% Pred. No. 2.04e+00;
Matches 15; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

Db 126 LVLNRPPLSLDHLDKLDVLMNVNPG-FG-GQATPGVLKVRQA 172

Qy 25 LKSSSDSELSWITELLEGKMAFOEALDPGPFDOGSPFAOELLDDGQA 73

RESULT 11
ID SPCA_HUMAN STANDARD; PRT: 2418 AA.
AC P02549; Q15514;
DT 21-JUL-1986 (REL. 01, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE SPECTRIN ALPHA CHAIN, ERYTHROCYTE.

GN SPTAL OR SPTA.
OS HOWO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE: 90170949.
RA SAHR K.E., LAURITA P., KOTULA L., SCARPA A.L., COUPAL E., LETO T.L.,
RA LINNENBACH A.J., WINKELMANN J.C., SPEICHER D.W., MARCHESI V.T.,
RA CURTIS P.J., FORGET B.G.;
RT "The complete cDNA and polypeptide sequences of human erythroid
RT alpha-spectrin."
RL J. BIOL. CHEM. 265:4434-4443(1990).

RN [2]
RP SEQUENCE OF 1-533 FROM N.A.
RX MEDLINE: 90009318.
RA SAHR K.E., TOBE T., SCARPA A., LAUGHINGHOUSE K., MARCHESI S.L.,
RA AGRE P., LINNENBACH A.J., MARCHESI V.T., FORGET B.G.;
RT "Sequence and exon-intron organization of the DNA encoding the alpha
RT I domain of human spectrin. Application to the study of mutations

RT causing hereditary elliptocytosis.";
 RL J. CLIN. INVEST. 84:1243-1252(1989).
 [13]
 RP SEQUENCE OF 7-601.
 RX MEDLINE: 84087888.
 RA SPEICHER D.W., DAVIS G., MARCHESI V.T.;
 RT "Structure of human erythrocyte spectrin. II. The sequence of the
 RT alpha-I domain.";
 RL J. BIOL. CHEM. 258:14938-14947(1983).
 [14]
 RP SEQUENCE OF 7-125.
 RX MEDLINE: 84087887.
 RA SPEICHER D.W., DAVIS G., YURCHENCO P.D., MARCHESI V.T.;
 RT "Structure of human erythrocyte spectrin. I. Isolation of the alpha-I
 RT domain and its cyanogen bromide peptides.";
 RL J. BIOL. CHEM. 258:14931-14937(1983).
 [15]
 RP SEQUENCE OF 320-450 FROM N.A.
 RX MEDLINE: 86205962.
 RA LINNENBACH A.J., SPEICHER D.W., MARCHESI V.T., FORGET B.G.;
 RT "Cloning of a portion of the chromosomal gene for human erythrocyte
 RT alpha-spectrin by using a synthetic gene fragment.";
 RL PROC. NATL. ACADE. SCI. U.S.A. 83:2397-2401(1986).
 [16]
 RP SEQUENCE OF 7-533 FROM N.A., AND VARIANT PRO-260; PRO-261 AND PRO-471.
 RX MEDLINE: 90009318.
 RA SAHR K.E., TOBE T., SCARPA A.L., LAUGHINGHOUSE K., MARCHESI S.L.,
 RA AGRE P., LINNENBACH A.J., MARCHESI V.T., FORGET B.G.;
 RT "Sequence and exon-intron organization of the DNA encoding the alpha
 RT I domain of human spectrin. Application to the study of mutations
 RT causing hereditary elliptocytosis.";
 RL J. CLIN. INVEST. 84:1243-1252(1989).
 [17]
 RP PARTIAL SEQUENCE.
 RX MEDLINE: 84295638.
 RA SPEICHER D.W., MARCHESI V.T.;
 RT "Erythrocyte spectrin is comprised of many homologous triple helical
 RT segments.";
 RL NATURE 311:177-180(1984).
 [18]
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 2407-2418.
 RA GIBSON T.J.;
 RL UNPUBLISHED OBSERVATIONS (MAR-1995).
 [19]
 RP REVIEW ON VARIANTS.
 RX MEDLINE: 97001215.
 RA MAILLET P., ALLOISIO N., MORLE L., DELAUNAY J.;
 RT "Spectrin mutations in hereditary elliptocytosis and hereditary
 RT spherocytosis.";
 RL HUM. MUTAT. 8:97-107(1996).
 [10]
 RP VARIANT SER-24.
 RX MEDLINE: 94289716.
 RA PARQUET N., DEVAUX I., BOULANGER L., GALAND C., BOIVIN P.,
 RA LECOMTE M.-C., DHERMY D., GARBARZ M.;
 RT "Identification of three novel spectrin alpha I/74 mutations in
 RT hereditary elliptocytosis: further support for a triple-stranded
 RT folding unit model of the spectrin heterodimer contact site.";
 RL BLOOD 84:303-308(1994).
 [11]
 RP VARIANTS CYS-28; HIS-28; LEU-28 AND SER-28.
 RX MEDLINE: 91358728.
 RA COETZER T.L., SAHR K., PRCHAL J., BLACKLOCK H., PETERSON L., KOLER R.,
 RA DOYLE J., MANASTER J., PALEK J.;
 RT "Four different mutations in codon 28 of alpha spectrin are
 RT associated with structurally and functionally abnormal spectrin alpha
 RT I/74 in hereditary elliptocytosis.";
 RL J. CLIN. INVEST. 88:743-748(1991).
 [12]
 RP VARIANTS SER-28 AND ARG-48.
 RX MEDLINE: 91346849.
 RA FLOYD P.B., GALLAGHER P.G., VALENTINO L.A., DAVIS M., MARCHESI S.L.,
 RA FORGET B.G.;

RT "Heterogeneity of the molecular basis of hereditary
 RT pyropoikilocytosis and hereditary elliptocytosis associated with
 RT increased levels of the spectrin alpha I/74-kilodalton tryptic
 RT peptide.";
 RL BLOOD 78:1364-1372(1991).
 [13]
 RP VARIANT SER-45.
 RX MEDLINE: 89323468.
 RA LECOMTE M.-C., GARBARZ M., GRANDCHAMP B., FEO C., GAUTERO H.,
 RA DEVAUX I., BOURNIER O., GALAND C., D'AURIOL L., GALIBERT F.,
 RA SAHR K.E., FORGET B.G., BOIVIN P., DHERMY D.;
 RT "Sp alpha I/78: a mutation of the alpha I spectrin domain in a white
 RT kindred with HE and HRP phenotypes.";
 RL BLOOD 74:1126-1133(1989).
 [14]
 RP VARIANT PRO-207.
 RX MEDLINE: 92176375.
 RA GALLAGHER P.G., TSE W.T., COETZER T., LECOMTE M.-C., GARBARZ M.,
 RA ZARKOWSKY H.S., BARUCHEL A., BALLAS S.K., DHERMY D., PALEK J.,
 RA FORGET B.G.;
 RT "A common type of the spectrin alpha I 46-50a-KD peptide abnormality
 RT in hereditary elliptocytosis and pyropoikilocytosis is associated
 RT with a mutation distant from the proteolytic cleavage site. Evidence
 RT for the functional importance of the triple helical model of
 RT spectrin.";
 RL J. CLIN. INVEST. 89:892-898(1992).
 [15]
 RP VARIANT VAL-1857.
 RX MEDLINE: 93253053.
 RA WILMOTTE R., MARECHAL J., MORLE L., BAKLOUTI F., PHILIPPE N.,
 RA KASTALLY R., KOTUJA L., DELAUNAY J., ALLOISIO N.;
 RT "Low expression allele alpha LEIX of red cell spectrin is associated
 RT with mutations in exon 40 (alpha V/41 polymorphism) and intron 45 and
 RT with partial skipping of exon 46.";
 RL J. CLIN. INVEST. 91:2091-2096(1993).
 [16]
 RP VARIANT BARCELONA.
 RX MEDLINE: 93572367.
 RA DALLA VENEZIA N., ALLOISIO N., FORISSIER A., DENOROV L., AYMERICH M.,
 RA VIVES-CORRONS J.L., BESALDUCH J., BESSON I., DELAUNAY J.;
 RT "Elliptocytosis associated with the alpha 469 His-->Pro
 RT mutation in spectrin Barcelona (alpha I/50-46b).";
 RL BLOOD 82:1661-1665(1993).
 [17]
 RP VARIANT CAGLIARI.
 RX MEDLINE: 94043025.
 RA SAHR K.E., COETZER T.L., MOY L.S., DERICK L.H., CHISHTI A.H.,
 RA JAROLIM P., LORENZO F., MIRAGLIA DEL GIUDICE E., IOLASCON A.,
 RA GALLANELLO R.;
 RT "Spectrin Cagliari: an Ala-->Gly substitution in helix 1 of beta
 RT spectrin repeat 17 that severely disrupts the structure and self-
 RT association of the erythrocyte spectrin heterodimer.";
 RL J. BIOL. CHEM. 268:22656-22662(1993).
 [18]
 RP VARIANTS CUILOZ AND LYON.
 RX MEDLINE: 90347052.
 RA MORLE L., ROUX A.-F., ALLOISIO N., POTHIER B., STARCK J., DENOROV J.,
 RA MORLE F., RUDIGOZ R.-C., FORGET B.G., DELAUNAY J., GOERT J.;
 RT "Two elliptocytogenic alpha I/74 variants of the spectrin alpha I
 RT domain. Spectrin Culoz (GGT-->GTT; alpha I 40 Gly-->Val) and
 RT spectrin Lyon (CTT-->TTT; alpha I 43 Leu-->Phe).";
 RL J. CLIN. INVEST. 86:548-554(1990).
 [19]
 RP VARIANT JENDOUBA.
 RX MEDLINE: 92345619.
 RA ALLOISIO N., WILMOTTE R., MORLE L., BAKLOUTI F., MARECHAL J.,
 RA DICUZZEAN M.-T., DENOROV L., FEO C., FORGET B.G., KASTALLY R.,
 RA DELAUNAY J.;
 RT "Spectrin Jendouba: an alpha II/31 spectrin variant that is
 RT associated with elliptocytosis and carries a mutation distant from
 RT the dimer self-association site.";
 RL BLOOD 80:809-815(1992).
 [20]

RP VARIANT TUNIS.
 RX MEDLINE: 89323436.
 RA MORIE L., MORIE F., ROUX A.F., GODET J., FORGET B.G., DENOROV L.,
 RA GABBAR M., DHERY D., KASTALLY R., DELAUNAY J.,
 RT "Spectrin Tunis (SP alpha I/78), an elliptocytogenic variant, is due
 to the CGG->TGG codon change (Arg->Tyr) at position 35 of the
 alpha I domain.".
 RL BLOOD 74:828-832(1989).
 RN [12]
 RP VARIANT GENOVA.
 RX MEDLINE: 94250920.
 RA PERROTTA S., DEL GUIDICE E.M., ALLOISIO N., SCIARRETTA G., PINTO L.,
 RT "Mild elliptocytosis associated with the alpha 34 Arg->Tyr mutation
 in spectrin genova (alpha I/74).".
 RL BLOOD 83:3346-3349(1994).
 RN [12]
 RP VARIANT ANASTASIA.
 RX MEDLINE: 95290423.
 RA PERROTTA S., IOLASCON A., DE ANGELIS F., PAGANO L., COLONNA G.,
 RA CURTILLO S., DEL GUIDICE E.M.,
 RT "Spectrin Anastasia (alpha I/78): a new spectrin variant (alpha 45
 Arg->Thr) with moderate elliptocytogenic potential.".
 RL BR. J. HAEMATOL. 89:933-936(1995).
 CC -I- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL
 NETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES
 WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF
 CC THE ERYTHROCYTE PLASMA MEMBRANE.
 CC ...
 Note: remainder of annotations omitted.

Query Match 14.7%; Score 88; DB 1; Length 2418;
 Best Local Similarity 31.3%; Pred. No. 2.04e+00;
 Matches 15; Conservative 15; Mismatches 15; Indels 3; Gaps 3;
 DB 1318 AEDLGIELLEH-QEHRADMEAPFOALEDSAEIISDGHASP 1364
 Oy 30 SDELSWTELEKDMARFOEALDP-GP-FDQGSFPAOELIDGQOASP 75

RESULT 12
 ID YDJA_ECOLI STANDARD; PRT: 183 AA.
 AC P24250:
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHEICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183).
 GN YDJA.
 OS ESCHERICHIA COLI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 OC ESCHERICHIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91317715.
 RA SAMERS G., HEIDER J., ZEHLEFEN E., BOECK A.,
 RT "Expression and operon structure of the sel genes of Escherichia coli
 and identification of a third selenium-containing formate
 dehydrogenase isoenzyme.".
 RL J. BACTERIOL. 173:4983-4993(1991).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RA MEDLINE: 97426617.
 RA BLATTNER F.R., PUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GODDEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.,
 RT "The complete genome sequence of Escherichia coli K-12.".
 RL SCIENCE 277:1453-1474(1997).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12.
 RX MEDLINE: 97251357.

RA AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,
 RA ITOH T., KASAI H., KASHIMOTO K., KIMURA S., KITARAWA M.,
 RA KITAGAWA M., MAKINO K., MIKI T., MIZOBUCHI K., MORI H., MORI T.,
 RA MOTOMURA K., NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y.,
 RA OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNARAM S.,
 RA TAGAMI H., TAKEDA J., TAKEKOTO K., TAKEUCHI Y., WADA C.,
 RA YAMAMOTO Y., HORIUCHI T.,
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.".
 RL DNA RES. 3:363-377(1996).
 CC -I- SIMILARITY: STRONG. TO H. INFLUENZAE H11542.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M68961; G147021; -
 DR EMBL: AE000271; G1788063; -
 DR EMBL: D90820; G1742876; -
 DR PIR: A40360; A40360.
 DR ECGENE: EG1134; YDJA.
 DR PFAM: PF00881; Nitroductase; 1.
 DR KW HYPOTHEICAL PROTEIN.
 SQ SEQUENCE 183 AA; 20059 MW; 6909542D CRC32;

Query Match 14.4%; Score 86; DB 1; Length 183;
 Best Local Similarity 26.9%; Pred. No. 3.63e+00;
 Matches 14; Conservative 15; Mismatches 20; Indels 3; Gaps 3;
 DB 20 APTGELONIRAGRAPDHKSMOPHFVEIGEREFSALDGAIAAGS 71
 Oy 12 GPLDQLAQLRD-LTSSSDBL-SWTELEKMGMA-FQALDPGPFDQGS 60

RESULT 13
 ID GRP3_ARTSA STANDARD; PRT: 308 AA.
 AC P13230:
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GLYCINE-RICH PROTEIN GRP33.
 OS ARTEMIA SALINA (BRINE SHRIMP).
 OC EUKARYOTA; METAZOA; ARTHROPODA; CRUSTACEA; BRANCHIOPODA; ANOSTRACA;
 OC ARTEMIIDAE; ARTEMIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88007550.
 RA CRUZ-ALVAREZ M., PELLICER A.,
 RT "Cloning of a full-length complementary DNA for an Artemia salina
 glycine-rich protein. Structural relationship with RNA binding
 proteins.".
 RL J. BIOL. CHEM. 262:13377-13380(1987).
 CC -I- SIMILARITY: TO HD40, THE MAJOR PROTEIN COMPONENT OF ARTEMIA
 CC HEMEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN PARTICLES, AND
 CC STRUCTURALLY TO OTHER NUCLEAR RNA BINDING PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J03453; G161174; -
 DR PIR: A29379; A29379.
 KW NUCLEAR PROTEIN; RIBONUCLEOPROTEIN; METHYLATION.
 FT DOMAIN 83 118 KH.

| | | | | | |
|--------------------------|---|---|-------------------------|-----------------|---------------------------------------|
| FT | DOMAIN | 186 | 308 | | GLY-RICH. |
| SQ | SEQUENCE | 308 AA: | 33034 MW: | 52ADCG73 CRC32: | |
| | | | | | |
| Query Match | | 14.4% | Score 86: | DB 1: | Length 308; |
| Best Local Similarity | | 34.7% | Pred. No. 3,63e+00: | | |
| Matches 17; Conservative | | 14; | Mismatches 15; | Indels | 3; Gaps 2; |
| | | | | | |
| Db | 203 | GPMSGRCGRGRCRGFGSGPD--RTFDLEKARNMTSEMDYGCFDES | 249 | | |
| Oy | 12 | GPLGQLHAQLRDLTSSSDLSLWIELLEKGMFGEALDGC-PRDCG | 59 | | |
| | | | | | |
| RESULT | 14 | STANDARD: | PRT: | 317 AA. | |
| ID | APE_PIG | PI8650: | 019099: | | |
| AC | 01-NOV-1990 | (REL. 16, | CREATED) | | |
| DT | 01-FEB-1994 | (REL. 28, | LAST SEQUENCE UPDATE) | | |
| DE | 15-DEC-1998 | (REL. 37, | LAST ANNOTATION UPDATE) | | |
| GN | APOE. | | | | |
| OS | SUS SCROFA (PIG). | | | | |
| OC | EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; | | | | |
| CC | ARTIODACTYLA; SUIFORMES; SUIDAE; SUS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE-LIVER: | | | | |
| RA | BROZOWSKA A.M., GRIMHOLT U., KUISETH M.A., WOLD I., ROGNE S.; | | | | |
| RL | SUBMITTED (MAY-1993) TO EMBL/GENBANK/DDBJ DATA BANKS. | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | RAMESONDAAR J.J., RUCKER E.B., VAZQUEZ J.C., PIEDRAHITA J.A.; | | | | |
| RL | SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. | | | | |
| RN | [3] | | | | |
| RP | PRELIMINARY SEQUENCE OF 19-31. | | | | |
| RX | MEDLINE: 81021043. | | | | |
| RA | "WEISGRABER K.H., TROXLER R.F., RALL S.C., MANLEY R.W.; | | | | |
| RT | "Comparison of the human, canine and swine epsilon apoproteins."; | | | | |
| RL | BIOCHEM. BIOPHYS. RES. COMMUN. 95:374-380(1980). | | | | |
| CC | -I- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM | | | | |
| CC | OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO | | | | |
| CC | B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON | | | | |
| CC | REMNANT) OF HEPATIC TISSUES. | | | | |
| CC | -I- SUBCELLULAR LOCATION: EXTRACELLULAR. | | | | |
| CC | -I- TISSUE SPECIFICITY: SECRETED IN PLASMA. | | | | |
| CC | -I- SIMILARITY: BELONGS TO THE APOAI / APOA4 / APOE FAMILY. | | | | |
| CC | ----- | | | | |
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| CC | the European Bioinformatics Institute. There are no restrictions on its | | | | |
| CC | use by non-profit institutions as long as their content is in no way com- | | | | |
| CC | modified and this statement is not removed. Usage by and for commercial | | | | |
| CC | entities requires a license agreement (see http://www.isb-sdb.ch/announce/a | | | | |
| CC | or send an email to license@isb-sdb.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL; X70235; G311233; " | | | | |
| DR | EMBL; U70240; G2388609; " | | | | |
| DR | PIR: A05312; A05312. | | | | |
| DR | PIR: S33450; S33450. | | | | |
| DR | HSPD; P02649; IOEF. | | | | |
| KW | GLYCOPROTEIN; PLASMA; LIPID TRANSPORT; HDL; VLDL; CHYLOMICRON; | | | | |
| KW | HEPARIN-BINDING; REPEAT; SIGNAL. | | | | |
| FT | SIGNAL | 1 | 18 | | |
| FT | CHAIN | 19 | 317 | | APOLIPOPROTEIN E. |
| FT | DOMAIN | 157 | 167 | | LDL RECEPTOR BINDING (POTENTIAL). |
| FT | DOMAIN | 161 | 164 | | HEPARIN-BINDING (BY SIMILARITY). |
| FT | DOMAIN | 228 | 235 | | HEPARIN-BINDING (BY SIMILARITY). |
| FT | DOMAIN | 79 | 254 | | 8 x 22 AA APPROXIMATE TANDEM REPEATS. |
| FT | REPEAT | 79 | 100 | | 1. |
| FT | REPEAT | 101 | 122 | | 2. |
| FT | REPEAT | 123 | 144 | | 3. |
| FT | REPEAT | 145 | 166 | | 4. |
| FT | REPEAT | 167 | 188 | | 5. |
| FT | REPEAT | 189 | 210 | | 6. |

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FT REPEAT      211    232       7.
FT CONFICT     233    254       8.
FT CONFICT     35     35       SV -> P (IN REF. 2).
FT CONFICT     160    161       NV -> KL (IN REF. 2).
FT CONFICT     166    166       V -> L (IN REF. 2).
FT CONFICT     251    252       DE -> EO (IN REF. 2).
FT CONFICT     273    273       A -> G (IN REF. 2).
FT CONFICT     275    275       O -> H (IN REF. 2).
FT CONFICT     277    277       R -> L (IN REF. 2).
FT CONFICT     289    289       M -> I (IN REF. 2).
FT CONFICT     303    303       A -> G (IN REF. 2).
SQ SEQUENCE    317 AA; 36599 MW; B/7IDA99 CRC32;.

Query Match          14.4% Score 86; DB 1; Length 317;
Best Local Similarity 28.4% Pred No. 3,636+00;
Matches      21; Conservative 23; Mismatches 26; Indels   4; Gaps   3;

Db      54 LRW-QSISDOVQEL--LSTKVOTELTELIESKYEKAYRELEA-QLGPVTOEQAR 109
        |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      7 LRLVGPRGDDDLHMDLRDLTSSSDLSMTIELLEKDMACFAOEALDPGDFGSPFAOEL 66
        |::||::||::||::||::||::||::||::||::||::||::||::||

Db      110 LSKELAQAARVGA 123
        |::||::||::||::||::||::||::||::||::||::||::||::||

OY      67 LDGGQAASPPHYGS 80

RESULT 15 STANDARD; PRT: 202 AA.
ID SODM_RABIT AC P41982;
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.1.1) (FRAGMENT).
GN SOD2.
OS ORCOTOLAGUS CUNICULUS (RABBIT).
OC EUMAROTA. METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
CC LAGOMORPHA: LEPORIDAE; ORCOTOLAGUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RA JACKSON R.M.;
RL SUBMITTED (xxx-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -I- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
CC -I- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -I- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
CC -----
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CC -----
CC DR EMBL; L28808; G454175; -.
DR PROSITE; PS00088; SOD_MN; 1.
DR PFAM; PF00081; sodfe; 1.
DR HSP; P04179; IMSD.
KW OXIDOREDUCTASE; MANGANESE; MITOCHONDRION; TRANSIT PEPTIDE.
FT NON_TER      1
FT TRANSIT      1
FT CHAIN        <1      5      MITOCHONDRION (BY SIMILARITY).
FT METAL         6    >202    SUPEROXIDE DISMUTASE, MANGANESE.
FT METAL        31    31      MANGANESE (BY SIMILARITY).
FT METAL        79    79      MANGANESE (BY SIMILARITY).
FT METAL       164   164      MANGANESE (BY SIMILARITY).
FT METAL       168   168      MANGANESE (BY SIMILARITY).
FT NON_TER      202
FT SEQUENCE     202 AA; 22656 MW; 3CBFFC2E CRC32;.

```


RP VARIANT TUNIS.
 RX MEDLINE: 89323436.
 RA MOLE L., MOLE F., ROUX A.F., GODET J., FORGET B.G., DENOROV L.,
 RA GABBAZ M., DHERRY D., KASTALLY R., DELAUNAY J.,
 RT "Spectrin Tunis (Sp alpha 1/78), an elliptocytogenic variant, is due
 to the CGG->TTC codon change (Arg->Tyr) at position 35 of the
 alpha I domain."
 RL BLOOD 74:828-832(1989).
 RN [21]
 RP VARIANT GENOVA.
 RX MEDLINE: 94250920.
 RA PEROTTA S., DEL GUIDICE E.M., ALLOISIO N., SCIARATTA G., PINTO L.,
 RA DELAUNAY J., CUTILLO S., IOLASCON A.,
 RT "Mild elliptocytosis associated with the alpha 34 Arg->Tyr mutation
 in spectrin genova (alpha 1/74)."
 RL BLOOD 83:3346-3349(1994).
 RN [22]
 RP VARIANT ANASTASIA.
 RX MEDLINE: 95290423.
 RA PEROTTA S., IOLASCON A., DE ANGELIS F., PAGANO L., COLONNA G.,
 RA CUTILLO S., DEL GUIDICE E.M.,
 RT "Spectrin Anastasia (alpha 1/78): a new spectrin variant (alpha 45
 Arg->Tyr) with moderate elliptocytogenic potential."
 RL BR. J. HAEMATOL. 89:933-936(1995).
 CC -I- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL
 NETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES
 WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF
 THE ERYTHROCYTE PLASMA MEMBRANE.
 CC
 Note: remainder of annotations omitted.

Query Match 14.7%; Score 88; DB 1; Length 2418;
 Best Local Similarity 31.3%; Pred. No. 2.04e+00;
 Matches 15; Conservative 15; Mismatches 15; Indels 3; Gaps 3;
 Db 1318 AEDLGIEILERH-QEHRADMEAPTEFOALEDSAEILDSGHASP 1364
 YQ 30 SDELWTELEKMGMAFOEALDP-GP-FDQSPFAOEILDGQDASP 75

RESULT 12
 ID YDJA.ECOLI STANDARD; PRT: 183 AA.
 AC P24250;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHEETICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183).
 GN YDJA.
 OS ESCHERICHIA COLI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 CC ESCHERICHIA.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91317715.
 RA SAVERS G., HEIDER J., ZEHLEIN E., BOECK A.,
 RT "Expression and operon structure of the sel genes of Escherichia coli
 and identification of a third selenium-containing formate
 dehydrogenase isoenzyme."
 RL J. BACTERIOL. 173:4983-4993(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-K12/MG1655;
 RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GODEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.,
 RT "The complete genome sequence of Escherichia coli K-12."
 RL SCIENCE 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE: 97251357.

RA AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,
 RA ITOH T., KASHI H., KASHIMOTO K., KIMURA S., KITAKAWA M.,
 RA KITAGAWA M., MARINO K., MIKI T., MIZOBACHI K., MORI H., MORI T.,
 RA MOTOMURA K., NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y.,
 RA OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SVASUNARAW S.,
 RA TAGAMI H., TAKEDA J., TAKEMOTO K., TAKEUCHI Y., WADA C.,
 RA YAMAMOTO Y., HORIUCHI T.,
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map."
 RL DNA RES. 3:363-377(1996).
 CC -I- SIMILARITY: STRONG, TO H. INFLUENZAE H11542.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC
 CC EMBL: M68961; G147021; -
 CC EMBL: AE000271; G1788063; -
 CC EMBL: D90820; G1742876; -
 CC PIR: A40360; A40360.
 CC ECGENE: EG11134; YDJA.
 CC PFAM: PF00881; Nitroreductase; 1.
 CC DR
 CC KW
 CC SEQUENCE 183 AA; 20059 MW; 6909542D CRC32;
 SQ

Query Match 14.4%; Score 86; DB 1; Length 183;
 Best Local Similarity 26.9%; Pred. No. 3.63e+00;
 Matches 14; Conservative 15; Mismatches 20; Indels 3; Gaps 3;
 Db 20 APTGEOLNIIRAGMARPDHRSKMPWFVEYEGGEREFSVILGCAIAGS 71
 YQ 12 GPLDQLHQAQRD-LTSSSDSL-SWTELEKMGMA-FOEALDPGRDQS 60

RESULT 13
 ID GRP3.ARTSA STANDARD; PRT: 308 AA.
 AC P13230;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GLYCINE-RICH PROTEIN GRP33.
 DE GLYCINE SALINA (BRINE SHRIMP).
 OS EURAROTA; METAZOA; ARTHROPODA; CRUSTACEA; BRANCHIOPODA; ANOSTRACA;
 CC ARTEMIDIAE; ARTEMIA.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88007550.
 RA CRUZ-ALVAREZ M., PELLICER A.,
 RT "Cloning of a full-length complementary DNA for an Artemia salina
 glycine-rich protein. Structural relationship with RNA binding
 proteins."
 RL J. BIOL. CHEM. 262:13377-13380(1987).
 CC -I- SIMILARITY: TO HD40, THE MAJOR PROTEIN COMPONENT OF ARTEMIA
 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN PARTICLES, AND
 STRUCTURALLY TO OTHER NUCLEAR RNA BINDING PROTEINS.
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 or send an email to license@isb-sib.ch).
 CC
 CC
 CC EMBL: J03453; G161174; -
 CC PIR: A29379; A29379.
 CC DR
 CC KW
 CC NUCLEAR PROTEIN; RIBONUCLEOPROTEIN; METHYLATION.
 CC DOMAIN 83 118 KH.

Tue. Oct. 26 15:35:01 1999

US-08-978-217-7.rsp

Page 9

| | | | | | |
|-----|-----------------------|---|----------------|------------|-------------|
| | Query Match | 14.2% | Score 85; | DB 1: | Length 202; |
| | Best Local Similarity | 25.0%; | Ped. No. | 4.82e+00; | |
| | Matches | 13; Conservative | 16; Mismatches | 21; Indels | 2; Gaps |
| Ddb | 8 | SLEPDPYGALEPHINNOIMELHSHKHA-AAYNNLNATEEK-YREPLANG | 57 | | |
| | | ::::: | ::::: | | |
| Oy | 3 | AEEIRLIVGFPGDDIQAOLNRTSSSDDELWITTEIKRDMGMAEQEKLIDRG | 54 | | |

Search completed: Thu Oct 21 16:30:14 1999
Job time : 29 secs.

